

Figure 1

Cr-449-tandem (4-amino acid linker between monomers is in double underline).

1	A	<u>CCG</u>	GTC	GCC	ACC	ATG	GTG	AGC	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	46
1	AgeI					M	V	S	G	L	L	K	E	S	M	R	11
47	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	94
12	I	K	M	Y	M	E	G	T	V	N	G	H	Y	F	K	C	27
95	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	142
28	E	G	E	G	D	G	N	P	F	A	G	T	Q	S	M	R	43
143	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	190
44	I	H	V	T	E	G	A	P	L	P	F	A	F	D	I	L	59
191	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	238
60	A	P	C	C	E	Y	G	S	R	T	F	V	H	H	T	A	75
239	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	286
76	E	I	P	D	F	F	K	Q	S	F	P	E	G	F	T	W	91
287	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	334
92	E	R	T	T	T	Y	E	D	G	G	I	L	T	A	H	Q	107
335	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	382
108	D	T	S	L	E	G	N	C	L	I	Y	K	V	K	V	L	123
383	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	430
124	G	T	N	F	P	A	D	G	P	V	M	K	N	K	S	G	139
431	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	478
140	G	W	E	P	S	T	E	V	V	Y	P	E	N	G	V	L	155
479	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	526
156	C	G	R	N	V	M	A	L	K	V	G	D	R	R	L	I	171
527	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	574
172	C	H	H	Y	T	S	Y	R	S	K	K	A	V	R	A	L	187
575	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	622
188	T	M	P	G	F	H	F	T	D	I	R	L	Q	M	L	R	203
623	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	670
204	K	E	K	D	E	Y	F	E	L	Y	E	A	S	V	A	R	219
671	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	AAC	<u>AGA TCT CCC GGG</u>	ATG	GTG	AGC				718
220	Y	S	D	L	P	E	K	A	N	R	S	P	G	M	V	S	235
719	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	766
236	G	L	L	K	E	S	M	R	I	K	M	Y	M	E	G	T	251
767	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	814
252	V	N	G	H	Y	F	K	C	E	G	E	G	D	G	N	P	267
815	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	862
268	F	A	G	T	Q	S	M	R	I	H	V	T	E	G	A	P	283
863	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	910
284	L	P	F	A	F	D	I	L	A	P	C	C	E	Y	G	S	299
911	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	958
300	R	T	F	V	H	H	T	A	E	I	P	D	F	F	K	Q	315
959	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	1006
316	S	F	P	E	G	F	T	W	E	R	T	T	T	Y	E	D	331
1007	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	1054
332	G	G	I	L	T	A	H	Q	D	T	S	L	E	G	N	C	347

FIGURE 1 (Cont)

1055	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	1102
348	L	I	Y	K	V	K	V	L	G	T	N	F	P	A	D	G	363
1103	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	1150
364	P	V	M	K	N	K	S	G	G	W	E	P	S	T	E	V	379
1151	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	1198
380	V	Y	P	E	N	G	V	L	C	G	R	N	V	M	A	L	395
1199	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	1246
396	K	V	G	D	R	R	L	I	C	H	H	Y	T	S	Y	R	411
1247	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	1294
412	S	K	K	A	V	R	A	L	T	M	P	G	F	H	F	T	427
1295	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	1342
428	D	I	R	L	Q	M	L	R	K	E	K	D	E	Y	F	E	443
1343	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	1390
444	L	Y	E	A	S	V	A	R	Y	S	D	L	P	E	K	A	459
1391	AAC	TGA															
460	N	*															

(SEQ ID NOS. 1&2)

Figure 2

Cr-449-tandem-actin (4-amino acid linker between Cr-449 monomers is noted in double underline; 4-amino acid linker between second Cr-449 and actin is noted in dashed underline).

1	A	<u>CCG</u>	GTC	GCC	ACC	ATG	GTG	AGC	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	46
1	AgeI					M	V	S	G	L	L	K	E	S	M	R	11
47	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	94
12	I	K	M	Y	M	E	G	T	V	N	G	H	Y	F	K	C	27
95	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	142
28	E	G	E	G	D	G	N	P	F	A	G	T	Q	S	M	R	43
143	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	190
44	I	H	V	T	E	G	A	P	L	P	F	A	F	D	I	L	59
191	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	238
60	A	P	C	C	E	Y	G	S	R	T	F	V	H	H	T	A	75
239	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	286
76	E	I	P	D	F	F	K	Q	S	F	P	E	G	F	T	W	91
287	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	334
92	E	R	T	T	T	Y	E	D	G	G	I	L	T	A	H	Q	107
335	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	382
108	D	T	S	L	E	G	N	C	L	I	Y	K	V	K	V	L	123
383	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	430
124	G	T	N	F	P	A	D	G	P	V	M	K	N	K	S	G	139
431	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	478
140	G	W	E	P	S	T	E	V	V	Y	P	E	N	G	V	L	155
479	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	526
156	C	G	R	N	V	M	A	L	K	V	G	D	R	R	L	I	171
527	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	574
172	C	H	H	Y	T	S	Y	R	S	K	K	A	V	R	A	L	187
575	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	622
188	T	M	P	G	F	H	F	T	D	I	R	L	Q	M	L	R	203
623	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	670
204	K	E	K	D	E	Y	F	E	L	Y	E	A	S	V	A	R	219
671	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	<u>AAC</u>	<u>AGA</u>	<u>TCT</u>	<u>CCC</u>	<u>GGG</u>	ATG	GTG	AGC	718
220	Y	S	D	L	P	E	K	A	N	R	S	P	G	M	V	S	235
719	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	766
236	G	L	L	K	E	S	M	R	I	K	M	Y	M	E	G	T	251
767	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	814
252	V	N	G	H	Y	F	K	C	E	G	E	G	D	G	N	P	267
815	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	862
268	F	A	G	T	Q	S	M	R	I	H	V	T	E	G	A	P	283
863	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	910
284	L	P	F	A	F	D	I	L	A	P	C	C	E	Y	G	S	299
911	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	958
300	R	T	F	V	H	H	T	A	E	I	P	D	F	F	K	Q	315
959	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	1006
316	S	F	P	E	G	F	T	W	E	R	T	T	T	Y	E	D	331

FIGURE 2 (CONT)

1007	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	1054
332	G	G	I	L	T	A	H	Q	D	T	S	L	E	G	N	C	347
1055	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	1102
348	L	I	Y	K	V	K	V	L	G	T	N	F	P	A	D	G	363
1103	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	1150
364	P	V	M	K	N	K	S	G	G	W	E	P	S	T	E	V	379
1151	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	1198
380	V	Y	P	E	N	G	V	L	C	G	R	N	V	M	A	L	395
1199	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	1246
396	K	V	G	D	R	R	L	I	C	H	H	Y	T	S	Y	R	411
1247	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	1294
412	S	K	K	A	V	R	A	L	T	M	P	G	F	H	F	T	427
1295	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	1342
428	D	I	R	L	Q	M	L	R	K	E	K	D	E	Y	F	E	443
1343	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	1390
444	L	Y	E	A	S	V	A	R	Y	S	D	L	P	E	K	A	459
1391	AAC	AGA	ACT	CGA	GCT	ATG	GAT	GAT	GAT	ATC	GCC	G...					1424
460	N	R	T	R	A	M	D	D	D	I	A...						470

actin

(SEQ ID NOS. 3&4).

FIGURE 3

HcRed-cr-1 tandem (4-amino acid linker between monomers is in double underline).

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ATGTCCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT
M S G L L K E S M R I K M Y M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
E G T V N G H Y F K C E G E G D G N P F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTCCTT
A G T Q S M R I H V T E G A P L P F A F

CGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
D I L A P C C E Y G S R T F V H H T A E

GATTCCCATTCTTCAAGCAGTCTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
I P D F F K Q S F P E G F T W E R T T T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAGTGCCT
Y E D G G I L T A H Q D T S L E G N C L

TATATACAAGGTGAAAGTCCATGGTACCAATTTTCTGCTGATGGCCCCGTGATGAAGAA
I Y K V K V H G T N F P A D G P V M K N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTGTG
K S G G W E P S T E V V Y P E N G V L C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCATTTGATCTGCCATCACTATAC
G R N V M A L K V G D R H L I C H H Y T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTCATTTTACAGA
S Y R S K K A V R A L T M P G F H F T D

CATCCGCCTTCAGATGCTGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
I R L Q M L R K K K D E Y F E L Y E A S

TGTGGCTAGGTACAGTGATCTTCTGAAAAAGCAAAAGA TCT CCC GGG
V A R Y S D L P E K A N R S P G

ATGTCCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT
M S G L L K E S M R I K M Y M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
E G T V N G H Y F K C E G E G D G N P F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTCCTT
A G T Q S M R I H V T E G A P L P F A F

CGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
D I L A P C C E Y G S R T F V H H T A E

GATTCCCATTCTTCAAGCAGTCTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
I P D F F K Q S F P E G F T W E R T T T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAGTGCCT
Y E D G G I L T A H Q D T S L E G N C L

TATATACAAGGTGAAAGTCCATGGTACCAATTTTCTGCTGATGGCCCCGTGATGAAGAA
I Y K V K V H G T N F P A D G P V M K N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTGTG
K S G G W E P S T E V V Y P E N G V L C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCATTTGATCTGCCATCACTATAC
G R N V M A L K V G D R H L I C H H Y T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTCATTTTACAGA
S Y R S K K A V R A L T M P G F H F T D
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FIGURE 3 (CONT)

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CATCCGCCTTCAGATGCTGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
I R L Q M L R K K K D E Y F E L Y E A S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
V A R Y S D L P E K A N *
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(SEQ ID NOS. 5 & 6)

FIGURE 4. AsRed-35-5NA tandem

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ATG GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
M A S L L T E T M P F R T T I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E G T V N G H Y F K C T G K G E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G N P L E G T Q E M K I E V I E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G G P L P F A F H I L S T S C M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y G S K A F I K Y V S G I P D Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F K Q S L P E G F T W E R T T T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y E D G G F L T A H Q D T S L D

GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC
G D C L V Y K V K I L G N N F P

GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC
A D G P V M Q N K A G R W E P S

ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC AGC
T E I V Y E V D G V L R G Q S S

ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC
M A L E C P G G R H L T C H L H

ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC
T T Y R S K K P A S A L K M P G

TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG
F H F E D H R I E I L E E V E K

GGC AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC GAC
G K C Y K Q Y E A A V G R Y C D

GCC GCC CCC TCC AAG CTG GGC CAC AAC AGA TCT CCC GGG
A A P S K L G H N R S P G

ATG GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
M A S L L T E T M P F R T T I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E G T V N G H Y F K C T G K G E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G N P L E G T Q E M K I E V I E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G G P L P F A F H I L S T S C M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y G S K A F I K Y V S G I P D Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F K Q S L P E G F T W E R T T T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y E D G G F L T A H Q D T S L D
```

Figure 4 (Cont)

```
GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC  
G D C L V Y K V K I L G N N F P  
GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC  
A D G P V M Q N K A G R W E P S  
ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC AGC  
T E I V Y E V D G V L R G Q S S  
ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC  
M A L E C P G G R H L T C H L H  
ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC  
T T Y R S K K P A S A L K M P G  
TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG  
F H F E D H R I E I L E E V E K  
GGC AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC GAC  
G K C Y K Q Y E A A V G R Y C D  
GCC GCC CCC TCC AAG CTG GGC CAC AAC  
A A P S K L G H N
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(SEQ ID NOS: 7 & 8)

FIGURE 5. AsRed-35-5D tandem

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GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
A S L L T E T M P F R T T I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E G T V N G H Y F K C T G K G E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G N P L E G T Q E M K I E V I E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G G P L P F A F H I L S T S C M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y G S K A F I K Y V S G I P D Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F K Q S L P E G F T W E R T T T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y E D G G F L T A H Q D T S L D

GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC
G D C L V Y K V K I L G N N F P

GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC
A D G P V M Q N K A G R W E P S

ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG
T E I V Y E V D G V L R G Q S L

ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC
M A L E C P G G R H L T C H L H

ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC
T T Y R S K K P A S A L K M P G

TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG
F H F E D H R I E I L E E V E K

GGC AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC GAC
G K C Y K Q Y E A A V G R Y C D

GCC GCC CCC TCC AAG CTG GGC CAC AAC AGA TCT CCC GGG
A A P S K L G H N R S P G

GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
A S L L T E T M P F R T T I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E G T V N G H Y F K C T G K G E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G N P L E G T Q E M K I E V I E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G G P L P F A F H I L S T S C M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y G S K A F I K Y V S G I P D Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F K Q S L P E G F T W E R T T T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y E D G G F L T A H Q D T S L D
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FIGURE 5 (CONT)

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GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC
G   D   C   L   V   Y   K   V   K   I   L   G   N   N   F   P

GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC
A   D   G   P   V   M   Q   N   K   A   G   R   W   E   P   S

ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG
T   E   I   V   Y   E   V   D   G   V   L   R   G   Q   S   L

ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC
M   A   L   E   C   P   G   G   R   H   L   T   C   H   L   H

ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC
T   T   Y   R   S   K   K   P   A   S   A   L   K   M   P   G

TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG
F   H   F   E   D   H   R   I   E   I   L   E   E   V   E   K

GGC AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC GAC
G   K   C   Y   K   Q   Y   E   A   A   V   G   R   Y   C   D

GCC GCC CCC TCC AAG CTG GGC CAC AAC
A   A   P   S   K   L   G   H   N
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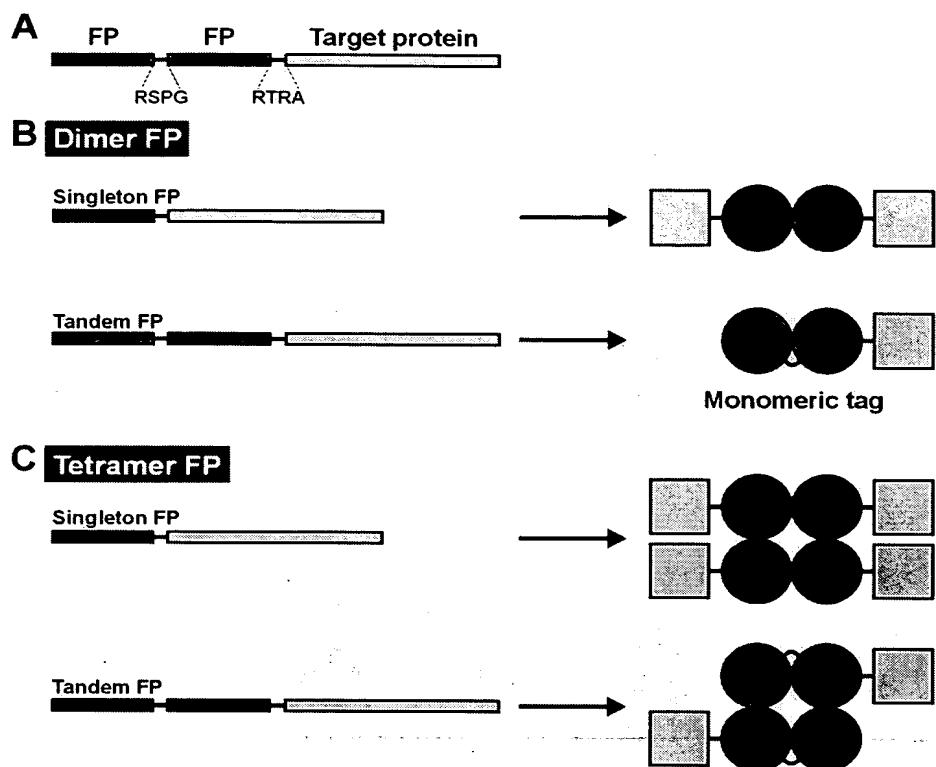


Figure 6

Figure 7. Comparison of various β -actin fusion constructs expressed in L929 fibroblasts.

<u>FPs fused to β-actin</u>	EGFP	HcRed2A	HcRed2A- tandem	DsRed2	DsRed2- tandem	M355NA	M355NA- tandem	HcRed	HcRed- tandem
Formation of aggregates	Very Low	Medium	Very low	High	Medium	High	Medium	High	Low
Labeling of actin structures	High	Medium	High	Very low	Medium	Very Low	High	Low	High
Cytoplasmic background	Low	Medium	Low	High	Low	High	Low	High	Low
Total overlay with EGFP	-	Medium	Very high	Very low	Medium	Very low	High	Low	High